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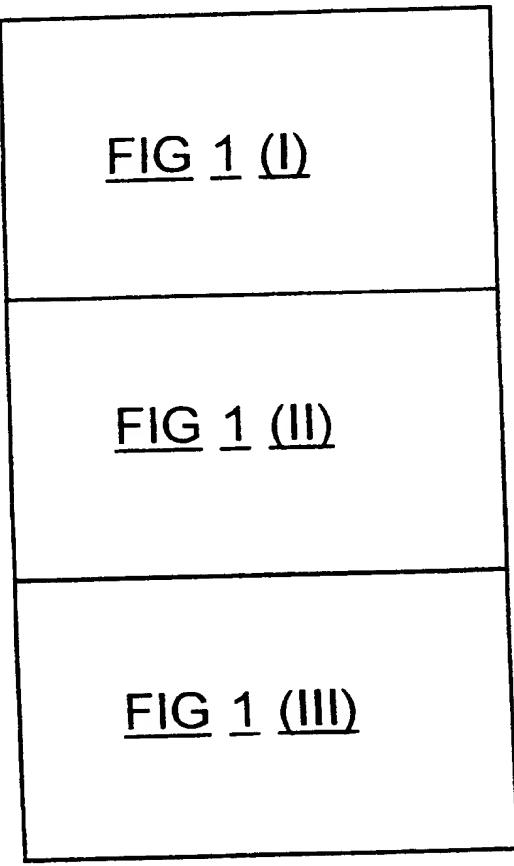


FIG 1 (I)

FIG 1 (II)

FIG 1 (III)

FIG 1

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FIGURE 1 (I)

GCCATCCAT CAACAGAAGG TTTAAGTGGG ATTCATTTTC ATTAGAAAAAG
96
ATCGGACAAA GGGTACTCTT AACCATACAA C ATG AGG GCG GTG GCG
5

GTT	TTC	TTT	GCT	TGC	GTT	CAC	AAA	GCC	138					
Val	Phe	Phe	Ala	Cys	Val	Leu	Phe	Cys	Met	Val	His	Lys	Ala	
GCA	CTT	GCG	GAT	GAT	AAA	ACG	TGC	AAC	CCT	ACA	GAT	TTT	ATG	180
Ala	Leu	Ala	Asp	Asp	Lys	Thr	Cys	Asn	Pro	Thr	Asp	Phe	Met	
GTT	ACC	CAA	ACC	ATA	ACT	GGA	TTG	ACA	ATC	GGC	GGT	AAA	CAA	222
Val	Thr	Gln	Ile	Thr	Ile	Gly	Leu	Thr	Ile	Gly	Gly	Lys	Gln	
GAG	TTC	GAG	GTC	AAT	TTA	ATA	AAC	AAT	TTG	TAT	TGT	GCA	CAA	264
Glu	Phe	Glu	Val	Asn	Leu	Ile	Asn	Asn	Leu	Tyr	Cys	Ala	Gln	

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FIGURE 1 (II)

TCT	AAT	GTC	AAA	GTT	TCA	TGT	GAC	GGG	CTT	CAT	ACC	ACC	GAA	306
Ser	Asn	Val	Lys	Val	Ser	Cys	Asp	Gly	Leu	His	Thr	Thr	Glu	75
CCA	ATA	GAT	CCT	CAC	ATT	ATC	AGA	CCA	CTT	AGT	GAC	GGA	ACG	348
Pro	Ile	Asp	Pro	His	Ile	Ile	Arg	Pro	Leu	Ser	Asp	Gly	Thr	85
AAC	AAC	TGC	CTT	GTC	AAC	AAT	GGA	GCG	CCT	ATT	TCT	CAT	GCT	390
Asn	Asn	Cys	Leu	Val	Asn	Asn	Gly	Ala	Pro	Ile	Ser	His	Ala	100
ACT	CTT	GTA	GCA	TTC	AAG	TAT	GCC	TGG	GAT	GTT	CCT	CCA	TCT	432
Thr	Leu	Val	Ala	Phe	Lys	Tyr	Ala	Trp	Asp	Val	Pro	Pro	Ser	115
TTC	AGC	ATC	ATC	AGC	TCT	GAT	ATA	AAT	TGC	TCC	TAA			468
Phe	Ser	Ile	Ile	Ser	Ser	Asp	Ile	Asn	Cys	Ser	OCH			125
GGAGAAA ATTCTAGTTG GCAGAGAATA ATCATATAGT CTTTTTTACT														515

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FIGURE 1 (III)

GAGCTATTAA ATTTCACCAA TTTTCACCAA TAAGATTATT TTAATGGAAT
565
GTTAAATGTAT TAGAATTGAA AAATAAAAAA AAAAAAAA AAAAAAAA
615
625
AAAAAAA

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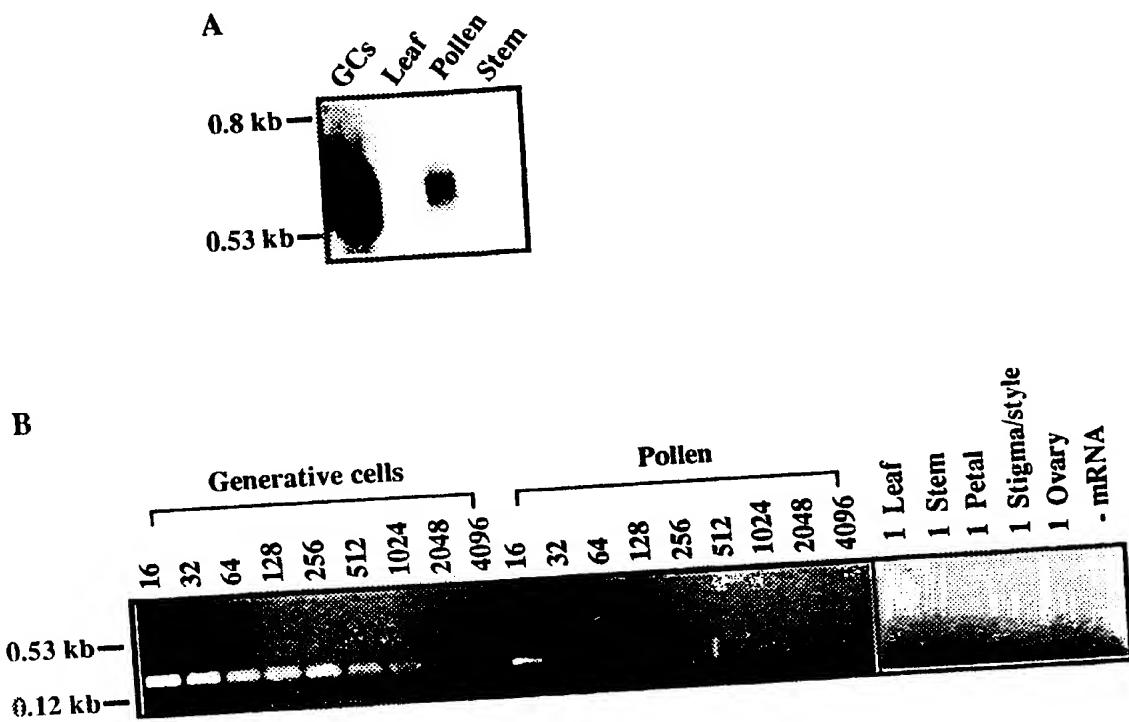


FIG 2

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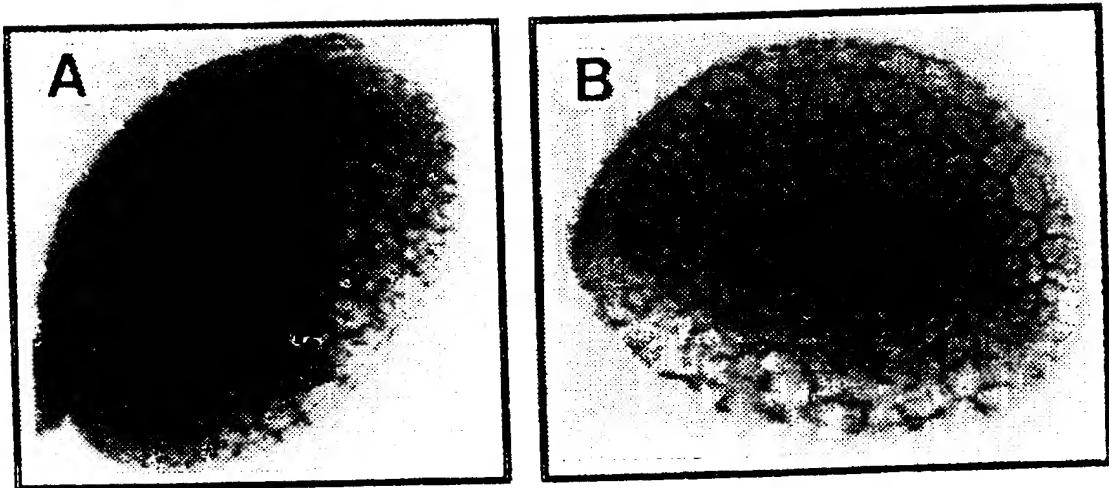


FIG 3

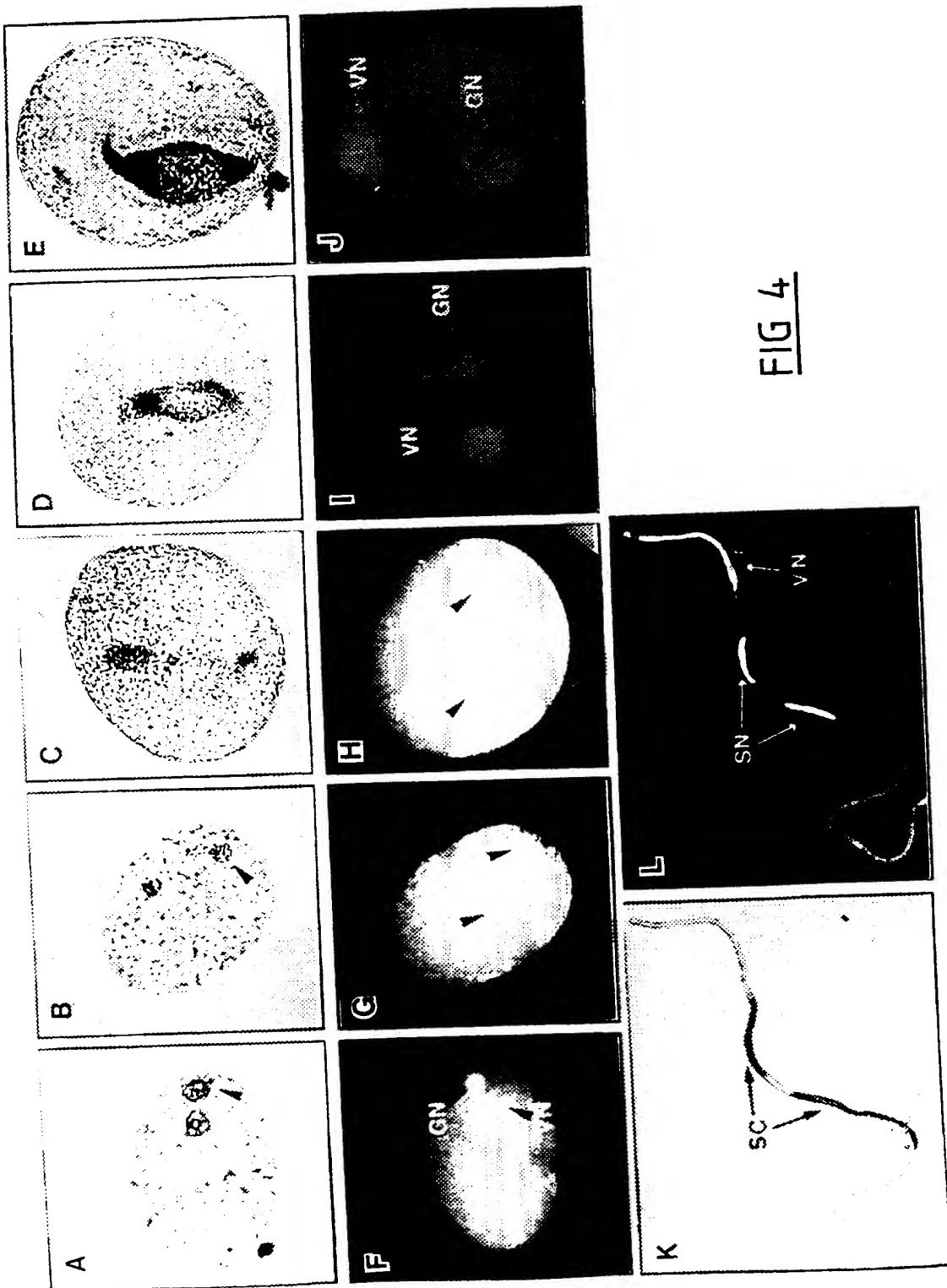


FIG 4

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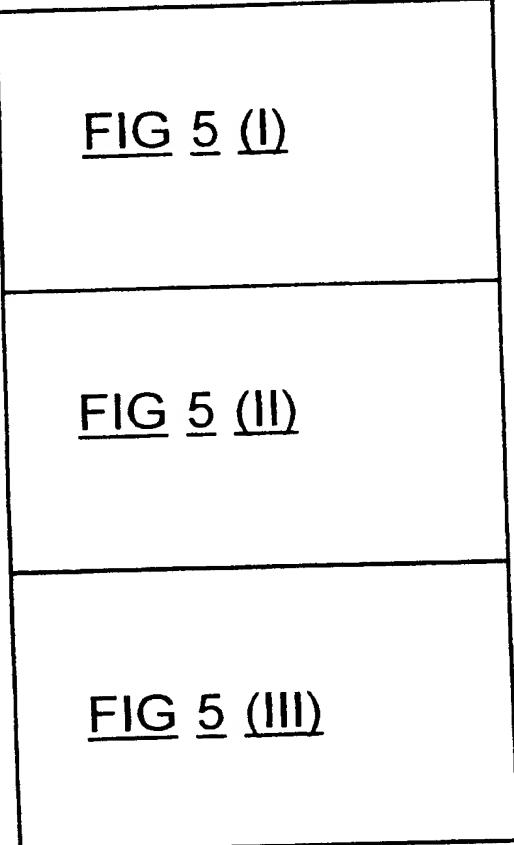


FIG 5 (I)

FIG 5 (II)

FIG 5 (III)

FIG 5

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FIGURE 5 (I)

GAAAGTGGAA	ACATCTCCAT	CAAACCTAG	AGTCAGATT	CCCACAAAG	48
ATG ATT TCA TCG GCA AAT AAC AAA GGC GCC GGC ACA AGC					87
Met Ile Ser Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser					
5					
CGC CGC AAG CTC CGT TCT GAG AAG GCT GCA CTC CAG TTC					126
Arg Arg Lys Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe					
15		20		25	
TCC GTC AGT CGC GTC GAA TAC TCC CTC AAG AAG GGG CGC					165
Ser Val Ser Arg Val Glu Tyr Ser Leu Lys Lys Gly Arg					
30		35			
TAT TGC AGG CGC TTA GGC GCT ACG GCC CCC GTC TAC CTA					204
Tyr Cys Arg Arg Leu G1Y Ala Thr Ala Pro Val Tyr Leu					
40		45		50	
GCC GCC GTG CTT GAA AAC CTC GTG GCC GAA GTG TTG GAC					243
Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp					
55		60			
65					

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FIGURE 5 (II)

ATG	GCG	GCG	AAC	GTG	ACA	GAA	GAA	TCC	CCC	ATT	GTT	282
Met	Ala	Ala	Asn	Val	Thr	Glu	Glu	Thr	Ser	Pro	Ile	Val
												75
												321
ATC	AAA	CCG	AGG	CAT	ATT	ATG	CTT	GCC	CCC	AGG	AAT	GAT
Ile	Lys	Pro	Arg	His	Ile	Met	Leu	Ala	Pro	Arg	Asn	Asp
												80
												85
GTA	GAA	GTT	GAA	CAA	GCT	GTT	TCA	CGG	TGT	CAC	CAT	CTC
Val	Glu	Val	Glu	Gln	Ala	Val	Ser	Arg	Cys	His	His	Leu
												95
												100
												360
GGC	ATC	AGG	TGT	CGT	CCC	TAAAACACGC	AAAGAGCTGG					398
Gly	Ile	Arg	Cys	Arg	Pro							110
												105
ACCGTCGCAA	ACGCCGTTCC	ACCTTTCAGC	CGGATTAGTT	CTTGATATT								448
CATTCTATCA	ATCTTGGTTA	TGTGACTGTG	ATTTTTCGTT	TTGTGTTGAA								498

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FIGURE 5 (III)

CTAAGCCCC TAATCTGGAT TTCTCGTTT ATGTTGAAC T AAGTCCTGTGC
ACTCTTGAAG TAAAAAAA AAAAAAAA AAAAAAAA 548
587

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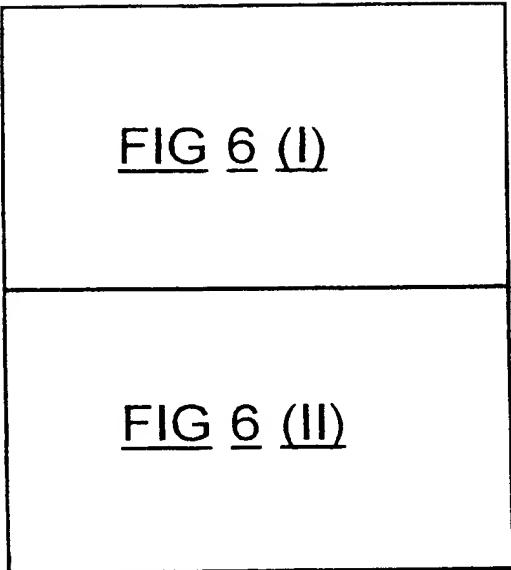


FIG 6 (I)

FIG 6 (II)

FIG 6

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FIGURE 6 (I)

GATCCCCAAAT	CATCA	ATG	ACG	ATC	CCC	GAA	AAG	AAA	TCC	GTC	42		
Met	Thr	Ile	Pro	Glu	Lys	Lys	Ser	Val					
1											5		
GCT	CCG	ATG	GCC	CGT	ATG	AAG	CAT	ACA	GCC	CGC	ATG	TCT	81
Ala	Pro	Met	Ala	Arg	Met	Met	Lys	His	Thr	Ala	Arg	Met	Ser
10													20
ACC	GGC	GGT	AAG	GCT	CCA	CGC	AAG	CAG	CTC	GCC	TCT	AAG	120
Thr	Gly	Gly	Lys	Ala	Pro	Arg	Lys	Gln	Leu	Ala	Ser	Lys	35
25													
GCT	CTT	CGC	AAG	GCG	CCA	CCA	CCA	CCG	ACC	AAA	GGA	GTG	159
Ala	Leu	Arg	Lys	Ala	Pro	Pro	Pro	Pro	Pro	Thr	Lys	Gly	Val
													45
AAG	CAG	CCC	ACC	ACT	ACC	TCC	GGA	AAA	TGG	CGC	TTC		198
Lys	Gln	Pro	Thr	Thr	Thr	Ser	Gly	Lys	Trp	Arg	Phe		60
50													

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FIGURE 6 (II)

GGC	AGA	TTT	CAC	AGG	AAA	CTG	CCA	TTC	CAA	GGG	CTG	GTG	237
Ala	Arg	Phe	His	Arg	Lys	Leu	Pro	Phe	Gln	Gly	Leu	Val	
65							70						
AGG	AAA	ATC	TGG	CAG	GAC	TTG	AAG	ACA	CAT	CTG	CGC	TTC	276
Arg	Lys	Ile	Trp	Gln	Asp	Leu	Lys	Thr	His	Leu	Arg	Phe	
75							80						
AAG	AAC	CAC	TCG	GTT	CCT	CCA	CTT	GAG	GAG	GTA	ACT	GAG	315
Lys	Asn	His	Ser	Val	Pro	Pro	Leu	Glu	Glu	Val	Thr	Glu	
							95					100	
GTT	TAT	CCT	TGC	CAA	ACT	ATT	GGA	GGA	TGC	TAT			348
Val	Tyr	Pro	Cys	Gln	Thr	Ile	Gly	Gly	Cys	Cys	Tyr		
							105						
TTGGATATTG	AATTGGATA	ATGGTTAAAT	TATCTGTTCT	ACCTTTATGA									398
TCAAATTTCT	GTGGCTCAGC	GTTGTGTAAT	TTGGGCAATC	GAATTCTTAG									448
CTATATTGCC	TCAAAAAAA	AAAAAA	AAAAAA	AAAAAA									485

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FIG 7

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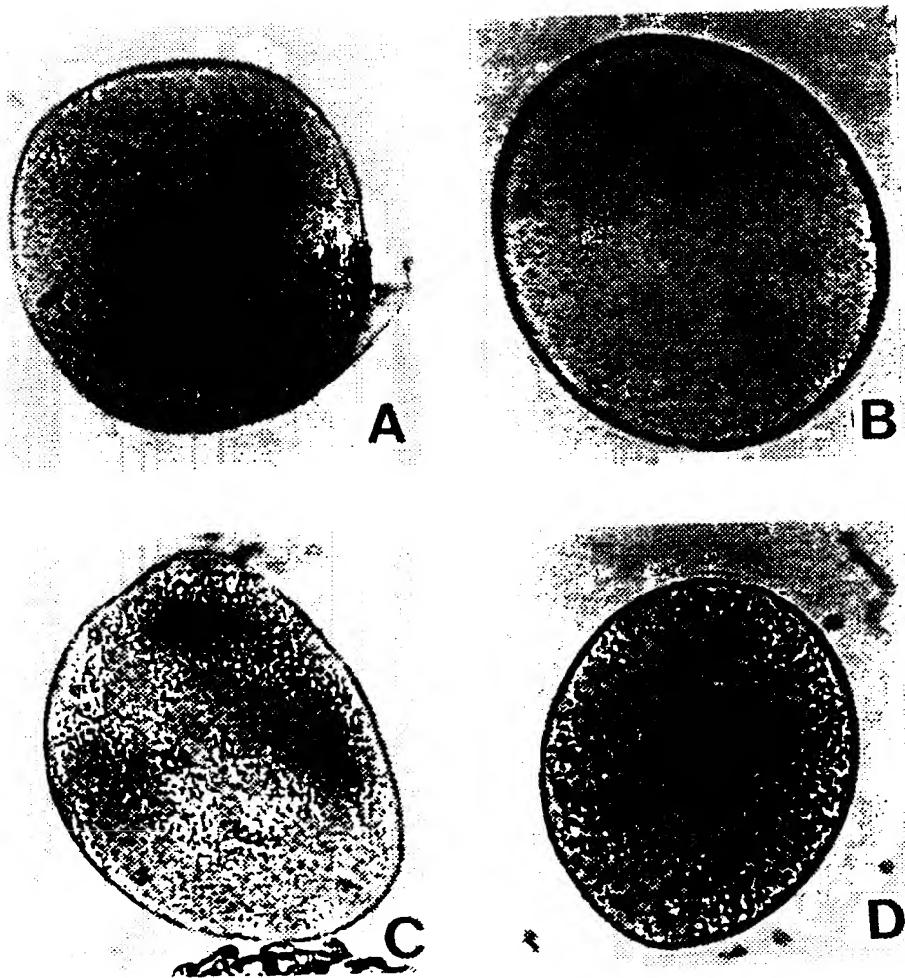


FIG 8

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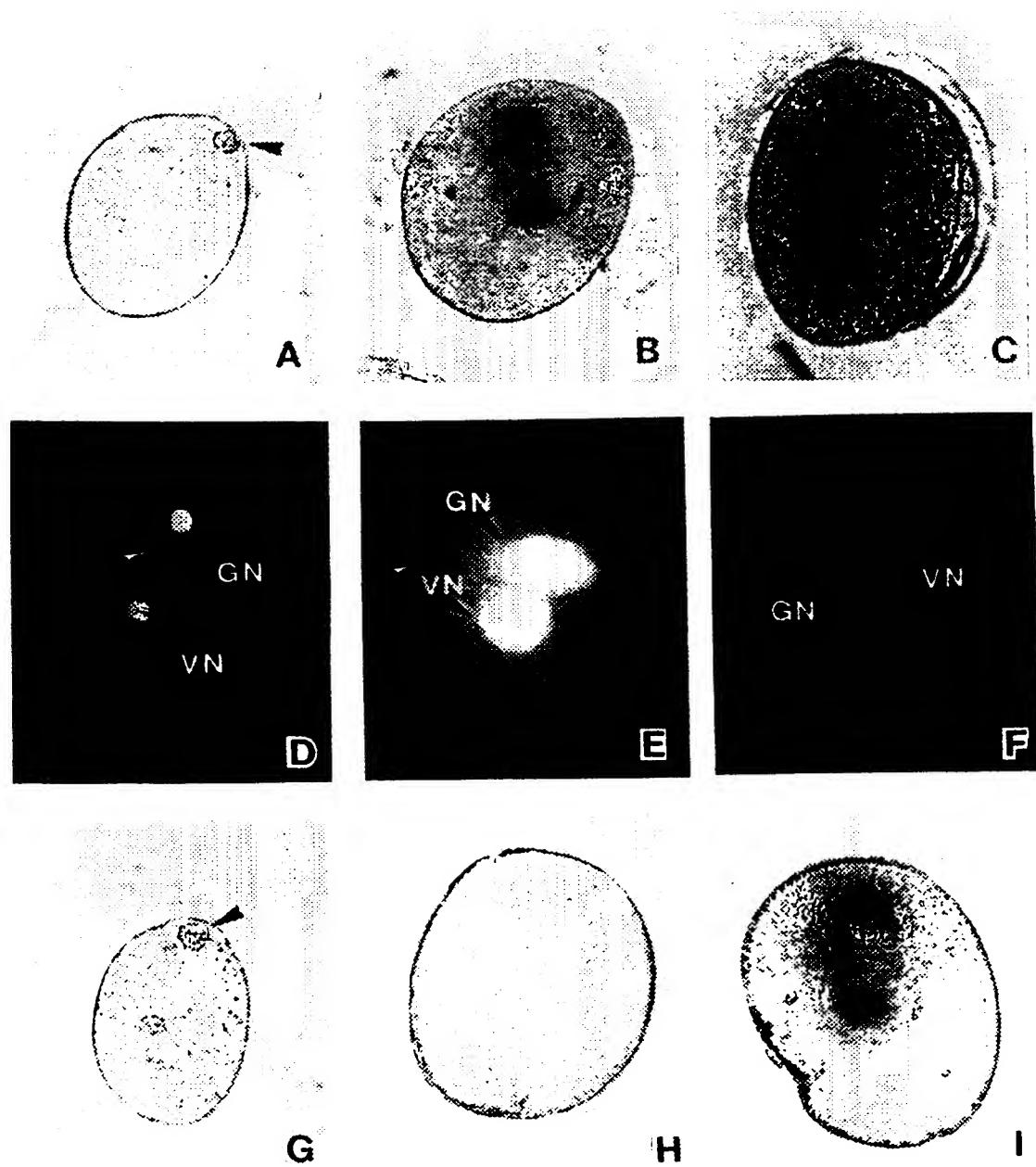


FIG 9

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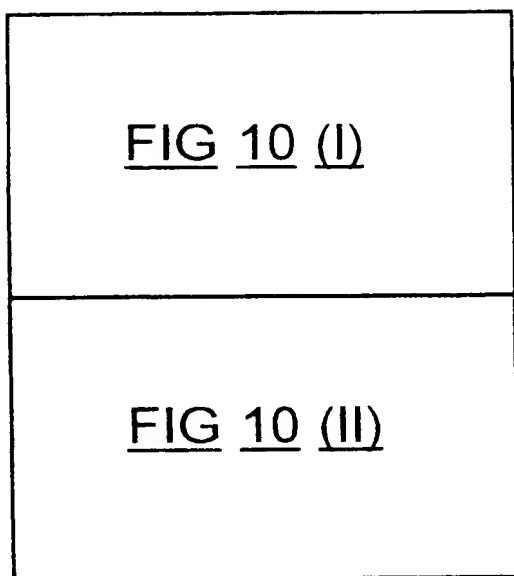


FIG 10

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FIGURE 10 (I)

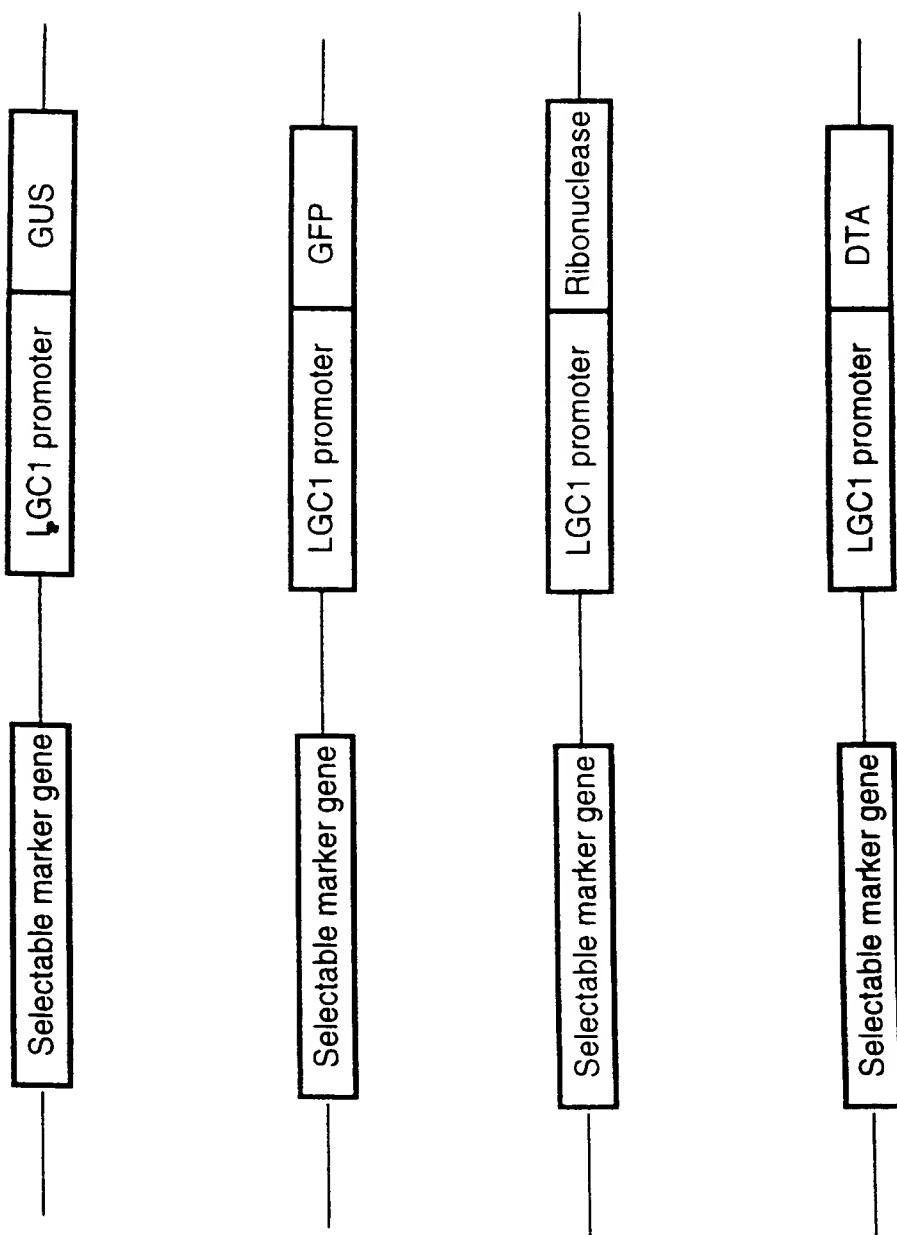
GGAGGGTGT	GGAATTAGGT	TTGCCCTAGG	TTTGCCCTAGG	TTTAGAGAAA	50
TAGTCAAAT	TGTCCCTATC	TATAAGGCATG	ATTTAGTAGT	GAGTTAATTAA	100
TCCCTATAATT	TCTCTTCTTG	TATGCTAAA	TAACCTGGTC	TTTAATGAAAT	150
AGATAATTAA	GTTTTGTAGC	AATTCTTCC	TCAAATTGAG	TATCAACAAAT	200
TGTTAGATTG	CTTTGGTGTAT	TATATTGAT	ATAATTGTT	GTAAGAAATGT	250
GTAGTGAAGAA	GATTGTGATT	ATTCAATTTCG	TTGTGTTGGACG	AATTGTTAGA	300
GCCCCATCGC	TAATGCCTTA	TAGTACTCGA	AATATGTTGG	GAATAGAAAGA	350
TGAAAATCC	CATTCTTTGT	AGTAGGAGTA	AAAATTGTC	TTTTCAATTAT	400
TCCATTGAAT	GTAAACCCT	TGCCATTCAAT	CTGACGGGA	TGGCAGAGTT	450
CCGACCATCT	AGTGATCCGT	GGGATATTGA	TTTTGGTGTG	TCAATGAAT	500
TGTGAGAACG	GGCTTCTGGG	AGAGAAAAGC	CCTCTTGCCT	CTGATATGAA	550
CACTGAGGCT	GATTATGTTA	ACGGATGGAG	ATTATTCAGT	GGCTGAATT	600
GGGTGCTGTA	GAGACAGAAT	TTGAAAGTT	TAACAATAAA	CCCTMATTCT	650
GAACCTGGGC	GGGGCTGGGA	TTTTACTCTT	AACGTGAAGA	GAGGCAAGAT	700
GAATTGACAG	CTTGGAAAGTC	GATCCAGTAT	TTGCAGCAGT	CGTGACGAAAT	750

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FIGURE 10 (II)

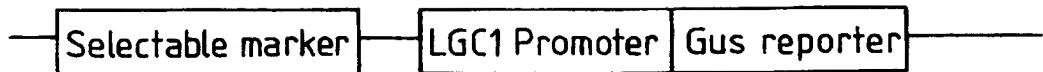
TGGTTGGACA	GTTACATCGG	TCAGAGAATG	CGTTCTATAA	ATTCCCCAA	800
TGGGGCAAGTG	AAAATCCCAT	CCCATCAACA	GAAGTTTTAA	GTGGAAACCC	850
ATTCCAATAG	AGAACGATCGA	ACAAAGGGTA	TTAACACATA	CAA <u>A</u> TGGGG	900
CAGTGGTGT	TCTTTTGCT	TGGCGTTCT	TCTGTATGGT	TCACAA	945

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FIG 11

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A



B

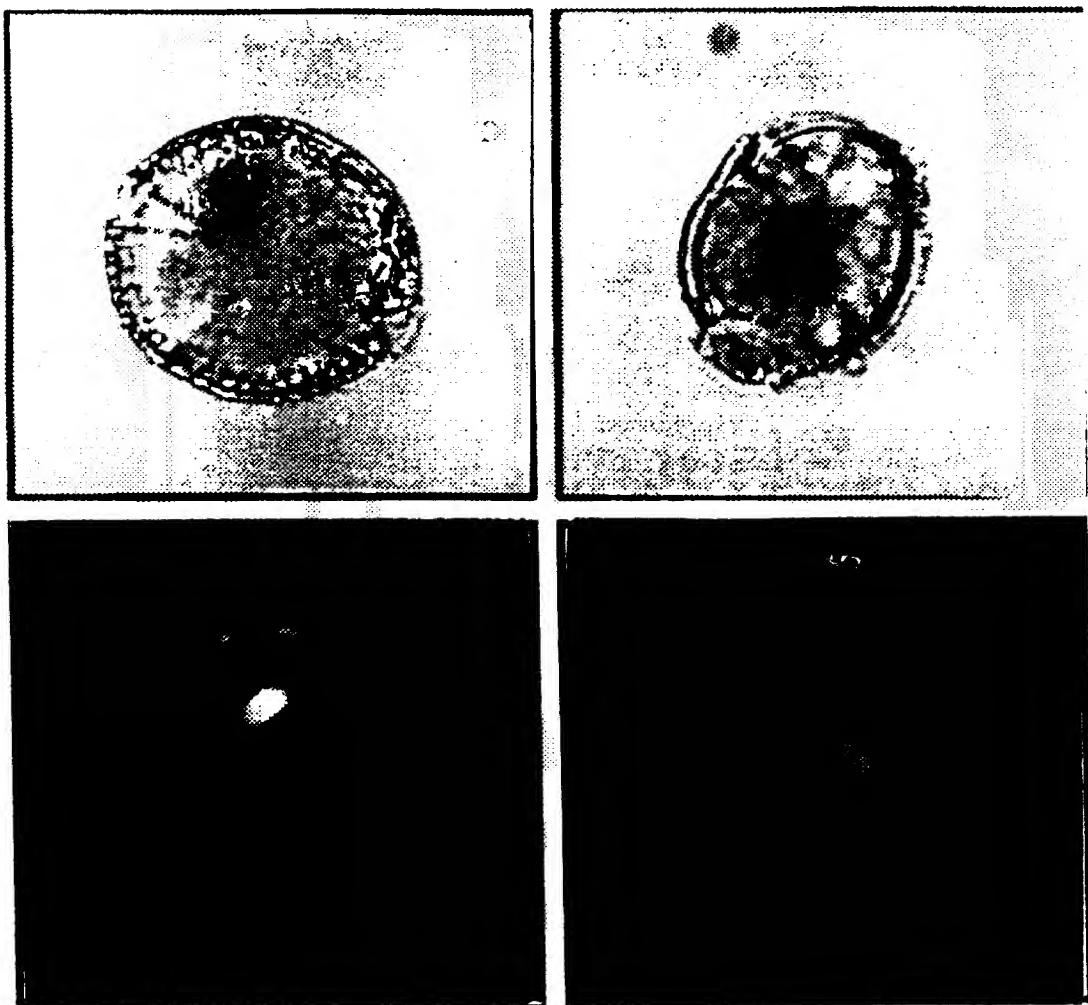


FIG 12